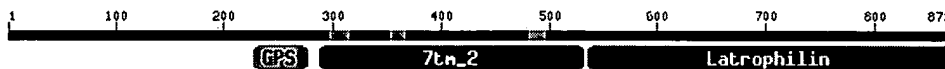


Your request has been successfully submitted and put into the Blast Queue.

Query = (872 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is

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Format

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Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by entrez query or select from:

Expect value range:

BLASTP 2.2.4 [Aug-26-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1032555785-026406-9303

Query=

(872 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

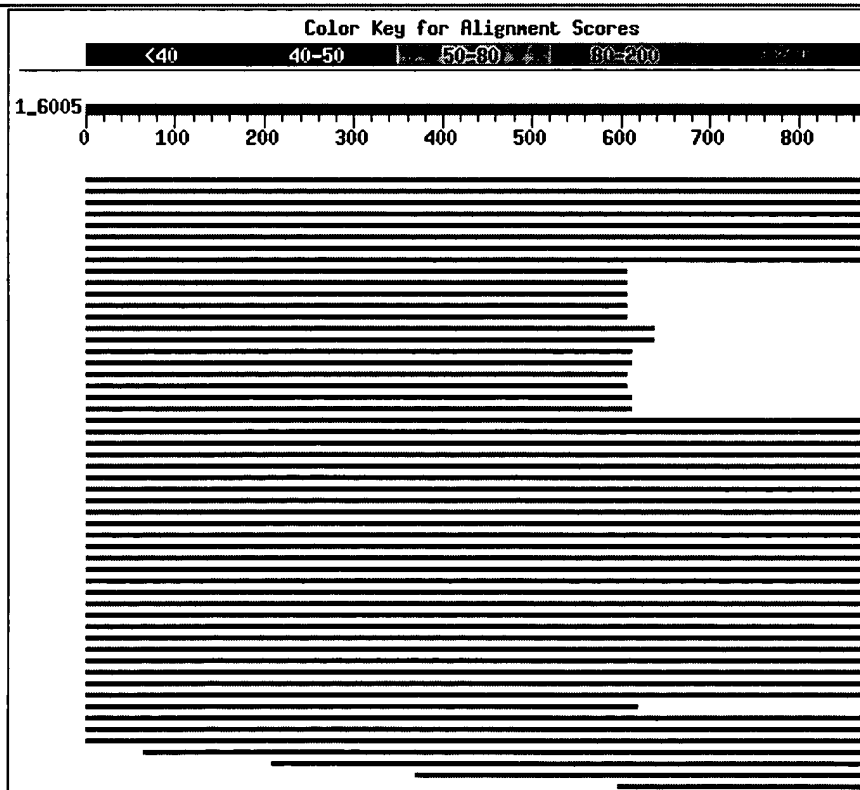
1,171,253 sequences; 370,891,306 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Score E
(bits) Value

Sequences producing significant alignments:

| | | | | | | | |
|----|----------|-----|-------------|---|------|-------|---|
| gi | 3882257 | dbj | BAA34488.1 | (AB018311) KIAA0768 protein [Hom... | 1659 | 0.0 | L |
| gi | 7513508 | pir | T18395 | latrophilin-3, splice variant bbaf, ... | 1623 | 0.0 | |
| gi | 7513502 | pir | T18389 | latrophilin-3, splice variant abaf, ... | 1620 | 0.0 | |
| gi | 7513949 | pir | T17198 | CL3BA protein - rat >gi 3695141 gb A... | 1618 | 0.0 | |
| gi | 7513511 | pir | T18407 | latrophilin-3, splice variant bbbf, ... | 1615 | 0.0 | |
| gi | 7513946 | pir | T17186 | CL3AA protein - rat >gi 3695135 gb A... | 1613 | 0.0 | |
| gi | 7513505 | pir | T18392 | latrophilin-3, splice variant abbf, ... | 1611 | 0.0 | |
| gi | 18677755 | ref | NP 570835.1 | (NM_130822) calcium-independen... | 1600 | 0.0 | L |
| gi | 7513950 | pir | T17199 | CL3BB protein - rat >gi 3695143 gb A... | 1118 | 0.0 | |
| gi | 7513947 | pir | T17187 | CL3AB protein - rat >gi 3695137 gb A... | 1116 | 0.0 | |
| gi | 14149677 | ref | NP 056051.1 | (NM_015236) lectomedin-3 [Homo... | 1116 | 0.0 | L |
| gi | 7513509 | pir | T18398 | latrophilin-3, splice variant bbag, ... | 1115 | 0.0 | |
| gi | 7513503 | pir | T18390 | latrophilin-3, splice variant abag, ... | 1115 | 0.0 | |
| gi | 7513951 | pir | T17200 | CL3BC protein - rat >gi 3695145 gb A... | 1113 | 0.0 | |
| gi | 7513510 | pir | T18405 | latrophilin-3, splice variant bbah, ... | 1112 | 0.0 | |
| gi | 7513948 | pir | T17188 | CL3AC protein - rat >gi 3695139 gb A... | 1112 | 0.0 | |
| gi | 7513504 | pir | T18391 | latrophilin-3, splice variant abah, ... | 1110 | 0.0 | |
| gi | 7513512 | pir | T18408 | latrophilin-3, splice variant bbbg, ... | 1107 | 0.0 | |
| gi | 7513506 | pir | T18393 | latrophilin-3, splice variant abbg, ... | 1107 | 0.0 | |
| gi | 7513513 | pir | T18409 | latrophilin-3, splice variant bbbh, ... | 1104 | 0.0 | |
| gi | 7513507 | pir | T18394 | latrophilin-3, splice variant abbh, ... | 1102 | 0.0 | |
| gi | 6912464 | ref | NP 036434.1 | (NM_012302) latrophilin 1; KIAA... | 925 | 0.0 | L |
| gi | 7513498 | pir | T18301 | latrophilin-2, splice variant baaae ... | 922 | 0.0 | |
| gi | 7513491 | pir | T18381 | latrophilin-2 (splice variant bbaae)... | 922 | 0.0 | |
| gi | 7513487 | pir | T18375 | latrophilin-2 (splice variant babae)... | 913 | 0.0 | |
| gi | 7513494 | pir | T18385 | latrophilin-2 (splice variant bbbae)... | 913 | 0.0 | |
| gi | 7513500 | pir | T18367 | latrophilin-2, splice variant baabe ... | 910 | 0.0 | |
| gi | 7513501 | pir | T18383 | latrophilin-2, splice variant bbabe ... | 908 | 0.0 | |
| gi | 7513489 | pir | T18379 | latrophilin-2 (splice variant babbe)... | 901 | 0.0 | |
| gi | 7513496 | pir | T18387 | latrophilin-2 (splice variant bbbbe)... | 900 | 0.0 | |
| gi | 7513499 | pir | T18366 | latrophilin-2, splice variant baaaf ... | 900 | 0.0 | |
| gi | 7513492 | pir | T18382 | latrophilin-2 (splice variant bbaaf)... | 899 | 0.0 | |
| gi | 7513942 | pir | T17158 | CL2AB protein - rat >gi 3695125 gb A... | 891 | 0.0 | |
| gi | 7513488 | pir | T18377 | latrophilin-2 (splice variant babaf)... | 891 | 0.0 | |
| gi | 7513495 | pir | T18386 | latrophilin-2 (splice variant bbbaf)... | 890 | 0.0 | |
| gi | 7513486 | pir | T18370 | latrophilin-2 (splice variant baabf)... | 887 | 0.0 | |
| gi | 3882293 | dbj | BAA34506.1 | (AB018329) KIAA0786 protein [Hom... | 887 | 0.0 | L |
| gi | 7513493 | pir | T18384 | latrophilin-2 (splice variant bbabf)... | 887 | 0.0 | |
| gi | 11280659 | pir | T46611 | CL2BB protein - rat >gi 3695131 gb ... | 879 | 0.0 | |
| gi | 7513490 | pir | T18380 | latrophilin-2 (splice variant babbf)... | 879 | 0.0 | |
| gi | 7513497 | pir | T18388 | latrophilin-2 (splice variant bbbbf)... | 878 | 0.0 | |
| gi | 7513943 | pir | T17159 | CL2AC protein - rat >gi 3695127 gb A... | 870 | 0.0 | |
| gi | 7513941 | pir | T17157 | CL2AA protein - rat >gi 3695123 gb A... | 862 | 0.0 | |
| gi | 7513945 | pir | T17185 | CL2BC protein - rat >gi 3695133 gb A... | 857 | 0.0 | |
| gi | 19705539 | ref | NP 599235.1 | (NM_134408) calcium-independen... | 852 | 0.0 | L |
| gi | 7513944 | pir | T17160 | CL2BA protein - rat >gi 3695129 gb A... | 849 | 0.0 | |
| gi | 5880490 | gb | AAD54675.1 | AF104266 1 (AF104266) lectomedin-1... | 736 | 0.0 | L |
| gi | 12621148 | ref | NP 075251.1 | (NM_022962) CL1BA protein [Rat... | 709 | 0.0 | L |
| gi | 7513937 | pir | T17138 | CL1AA protein - rat >gi 2213659 gb A... | 709 | 0.0 | |
| gi | 7513485 | pir | T18413 | latrophilin-1, brain-specific - bovi... | 702 | 0.0 | |
| gi | 7513484 | pir | T18411 | latrophilin-1, brain-specific - bovi... | 702 | 0.0 | |
| gi | 7662324 | ref | NP 055736.1 | (NM_014921) lectomedin-2; KIAA0... | 701 | 0.0 | L |
| gi | 11037014 | gb | AAG27461.1 | AF307079 1 (AF307079) lectomedin-... | 701 | 0.0 | L |
| gi | 7513940 | pir | T17156 | CL1BB protein - rat >gi 3695121 gb A... | 689 | 0.0 | |
| gi | 7513938 | pir | T17145 | CL1AB protein - rat >gi 3695117 gb A... | 689 | 0.0 | |
| gi | 5880492 | gb | AAD54676.1 | AF104938 1 (AF104938) lectomedin-1... | 677 | 0.0 | L |
| gi | 14043198 | gb | AAH07587.1 | AAH07587 (BC007587) Unknown (prot... | 643 | 0.0 | L |
| gi | 20885613 | ref | XP 134383.1 | (XM_134383) similar to CL1BA p... | 523 | e-147 | L |
| gi | 20878925 | ref | XP 131258.1 | (XM_131258) similar to phospho... | 503 | e-141 | L |
| gi | 20835942 | ref | XP 144383.1 | (XM_144383) similar to beta-ca... | 494 | e-138 | L |

| | | | | | | | | |
|----|----------|-----|-------------|--------------------------------|---------------------------------|-----|-------|---|
| gi | 11545908 | ref | NP_071442.1 | (NM_022159) | EGF-TM7-latrophili... | 311 | 2e-83 | L |
| gi | 18875378 | ref | NP_573485.1 | (NM_133222) | ETL1 [Mus musculus... | 300 | 5e-80 | L |
| gi | 16877798 | gb | AAH17134.1 | (BC017134) | Unknown (protein for ... | 299 | 1e-79 | L |
| gi | 20879033 | ref | XP_124185.1 | (XM_124185) | similar to ETL1 [M... | 299 | 1e-79 | L |
| gi | 11560111 | ref | NP_071630.1 | (NM_022294) | ETL protein [Rattu... | 287 | 6e-76 | L |
| gi | 20835937 | ref | XP_144382.1 | (XM_144382) | similar to calcium... | 237 | 4e-61 | L |
| gi | 9663052 | emb | CAC01096.1 | (AJ272270) | 110-R orphan receptor... | 228 | 2e-58 | |
| gi | 14211883 | ref | NP_115960.1 | (NM_032571) | EGF-like module-co... | 227 | 5e-58 | L |
| gi | 15528829 | gb | AAK51125.1 | (AY032690) | EGF-like module-conta... | 223 | 1e-56 | L |
| gi | 20982827 | ref | NP_631877.1 | (NM_139138) | F4/80-like-recepto... | 223 | 1e-56 | L |
| gi | 20900604 | ref | XP_128711.1 | (XM_128711) | EGF-like module co... | 215 | 2e-54 | L |
| gi | 17978489 | ref | NP_001775.2 | (NM_001784) | CD97 antigen, isof... | 212 | 2e-53 | L |
| gi | 17978491 | ref | NP_510966.1 | (NM_078481) | CD97 antigen, isof... | 211 | 3e-53 | L |
| gi | 1685051 | gb | AAB36682.1 | (U76764) | CD97 [Homo sapiens] | 211 | 3e-53 | L |
| gi | 19170724 | emb | CAC94754.1 | (AJ416058) | CD97 protein [Bos ta... | 211 | 3e-53 | |
| gi | 21929208 | dbj | BAC06178.1 | (AB065966) | seven transmembrane ... | 211 | 4e-53 | |
| gi | 17531351 | ref | NP_495894.1 | (NM_063493) | G-protein coupled ... | 210 | 6e-53 | L |
| gi | 11225481 | gb | AAG33020.1 | (AF192402) | ETL protein [Rattus n... | 209 | 1e-52 | L |
| gi | 2135556 | pir | I37225 | leucocyte antigen CD97 - human | >gi 8... | 207 | 7e-52 | |
| gi | 6226566 | sp | P48960 | CD97 HUMAN | Leucocyte antigen CD97 prec... | 206 | 1e-51 | |
| gi | 7305025 | ref | NP_038475.1 | (NM_013447) | egf-like module con... | 198 | 3e-49 | L |
| gi | 21929123 | dbj | BAC06146.1 | (AB065931) | seven transmembrane ... | 197 | 4e-49 | |
| gi | 22024081 | ref | NP_610397.2 | (NM_136553) | CG8639 gene produc... | 192 | 1e-47 | L |
| gi | 4469185 | emb | CAB38413.1 | (AL031588) | dJ1163J1.1 (mostly su... | 192 | 2e-47 | L |
| gi | 7656967 | ref | NP_055061.1 | (NM_014246) | cadherin EGF LAG se... | 191 | 4e-47 | L |
| gi | 2935597 | gb | AAC05172.1 | (AC004262) | R29368_2 [Homo sapiens] | 191 | 5e-47 | L |
| gi | 6753408 | ref | NP_034016.1 | (NM_009886) | cadherin EGF LAG se... | 188 | 3e-46 | L |
| gi | 7021080 | dbj | BAA91375.1 | (AK000781) | unnamed protein produ... | 185 | 2e-45 | |
| gi | 15638633 | gb | AAL05061.1 | AF413207_1 | (AF413207) CD97 antige... | 181 | 3e-44 | |
| gi | 21929097 | dbj | BAC06133.1 | (AB065918) | seven transmembrane ... | 180 | 7e-44 | |
| gi | 4503565 | ref | NP_001965.1 | (NM_001974) | egf-like module con... | 177 | 4e-43 | L |
| gi | 22095545 | sp | Q9QYP2 | CLR2 RAT | Cadherin EGF LAG seven-pass ... | 176 | 9e-43 | |
| gi | 7707357 | gb | AAF67800.1 | AF146344_1 | (AF146344) CD97 antigen... | 174 | 6e-42 | L |
| gi | 13529572 | gb | AAH05499.1 | (BC005499) | Unknown (protein for ... | 174 | 6e-42 | L |
| gi | 12835843 | dbj | BAB23386.1 | (AK004577) | CD97 antigen-data so... | 173 | 9e-42 | L |
| gi | 13879392 | gb | AAH06676.1 | (BC006676) | Similar to CD97 antig... | 173 | 9e-42 | L |
| gi | 1665821 | dbj | BAA13407.1 | (D87469) | Similar to D.melanogast... | 173 | 1e-41 | L |
| gi | 13325064 | ref | NP_001399.1 | (NM_001408) | cadherin EGF LAG s... | 172 | 1e-41 | L |
| gi | 22095553 | sp | Q9ROM0 | CLR2 MOUSE | Cadherin EGF LAG seven-pas... | 172 | 2e-41 | |
| gi | 11995466 | ref | NP_059088.1 | (NM_017392) | cadherin EGF LAG s... | 171 | 3e-41 | L |

Alignments

Get selected sequences

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☐ >gi|3882257|dbj|BAA34488.1| (AB018311) KIAA0768 protein [Homo sapiens]
Length = 872

Score = 1659 bits (4296), Expect = 0.0

Identities = 818/872 (93%), Positives = 818/872 (93%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKAMVETVNNLLQP 60

AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKAMVETVNNLLQP

Sbjct: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKAMVETVNNLLQP 60

Query: 61 QALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120

QALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG

Sbjct: 61 QALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120

Query: 121 NLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYLSTENASMKLGTEA 180
 NLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYLSTENASMKLGTEA
 Sbjct: 121 NLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYLSTENASMKLGTEA 180

Query: 181 LSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFNPNCFSWSYSKRTM 240
 LSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFNPNCFSWSYSKRTM
 Sbjct: 181 LSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFNPNCFSWSYSKRTM 240

Query: 241 TGYWSTNGCRLLTTNKTHTTTCSCNHLTNFAVLMAHVEVKHSDAVHDLDDLVDITWVGXXXX 300
 TGYWST GCRLLTTNKTHTTTCSCNHLTNFAVLMAHVEVKHSDAVHDLDDLVDITWVG
 Sbjct: 241 TGYWSTQGCRLLTTNKTHTTTCSCNHLTNFAVLMAHVEVKHSDAVHDLDDLVDITWVGILLS 300

Query: 301 XXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTDQPIACXXXXXXXXX 360
 RGL SDRNTIHKNLCSL FVAELLFLIGINRTDQPIAC
 Sbjct: 301 LVCLLICIFTFCFFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTDQPIACAVFAALLH 360

Query: 361 XXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIVAVSAADVRSYGT 420
 TWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIVAVSAADVRSYGT
 Sbjct: 361 FFFLAATWWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIVAVSAADVRSYGT 420

Query: 421 DKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKPESGCLDNIKSWVI 480
 DKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKPESGCLDNIKSWVI
 Sbjct: 421 DKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKPESGCLDNIKSWVI 480

Query: 481 XXXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHCVLQKKVRKEYGKC 540
 MYINESTVIMAYLFTIFNSL GMFIFIFHCVLQKKVRKEYGKC
 Sbjct: 481 GAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRKEYGKC 540

Query: 541 LRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIRRMWNDTVRKQSESSFITGDINS 600
 LRTHCCSGKSTESSIGSGKTSGRTPGRYSTGS SRIRRMWNDTVRKQSESSFITGDINS
 Sbjct: 541 LRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSQSRIRRMWNDTVRKQSESSFITGDINS 600

Query: 601 SASLNREGLLNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEK 660
 SASLNREGLLNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEK
 Sbjct: 601 SASLNREGLLNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEK 660

Query: 661 KILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLG 720
 KILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLG
 Sbjct: 661 KILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLG 720

Query: 721 LELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLL TNEHTEDLQSPHRDS 780
 LELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLL TNEHTEDLQSPHRDS
 Sbjct: 721 LELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLL TNEHTEDLQSPHRDS 780

Query: 781 LYTSMP TLAGVAATESVTTSTQT EPPPAKCGDAEDVYYKSM PNLGSRNHVHQLHTYYQLG 840
 LYTSMP TLAGVAATESVTTSTQT EPPPAKCGDAEDVYYKSM PNLGSRNHVHQLHTYYQLG
 Sbjct: 781 LYTSMP TLAGVAATESVTTSTQT EPPPAKCGDAEDVYYKSM PNLGSRNHVHQLHTYYQLG 840

Query: 841 RGSSDGFIVPPNKDGT PPEGSSKGAHLVTSL 872
 RGSSDGFIVPPNKDGT PPEGSSKGAHLVTSL
 Sbjct: 841 RGSSDGFIVPPNKDGT PPEGSSKGAHLVTSL 872

☐ >gi|7513508|pir||T18395 latrophilin-3, splice variant bbaf, brain-specific - bov
 gi|4164065|gb|AAD05327.1| (AF111091) latrophilin 3 splice variant bbaf [Bos tauru
 Length = 1571

Score = 1623 bits (4202), Expect = 0.0
 Identities = 807/928 (86%), Positives = 810/928 (86%), Gaps = 56/928 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK
 Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVMNLLQPQALNAWRDLTTS DQLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107

AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 763
 Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
 NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
 Sbjct: 764 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 823
 Query: 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
 STENASMKLGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
 Sbjct: 824 STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 883
 Query: 228 PNCSEFWSYSKRTMTGYWSTNGCRLLTTNKTHHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 287
 PNCSEFWSYSKRTMTGYWST GCRLLTTNKTHHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL
 Sbjct: 884 PNCSEFWSYSKRTMTGYWSTQGCRLLTTNKTHHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 943
 Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
 LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD
 Sbjct: 944 LLDVITWVGILLSLVCLLICITFCFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 1003
 Query: 348 QPIACXXXXXXXXXXXXXXXXXTW MFLEGVQLYIMLVEVFESEHSRRKYFYLVGYGMPALIV 407
 QPIAC TW MFLEGVQLYIMLVEVFESEHSRRKYFYLVGYGMPALIV
 Sbjct: 1004 QPIACAVFAALLHFFFLAAFTW MFLEGVQLYIMLVEVFESEHSRRKYFYLVGYGMPALIV 1063
 Query: 408 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 467
 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP
 Sbjct: 1064 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 1123
 Query: 468 ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
 ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
 Sbjct: 1124 ESGCLDNIKSWVIGAIALLCLLGLT WAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1183
 Query: 528 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIRRMWNDTVRK 587
 VLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTSGRTPGRYSTGS SRIRRMWNDTVRK
 Sbjct: 1184 VLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTSGRTPGRYSTGSQSRIIRRMWNDTVRK 1243
 Query: 588 QSESSFITGDINSSASLNR----- 606
 QSESSFITGDINSSASLNR
 Sbjct: 1244 QSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNNPYN TLLGEPAVCNNPSVSMYN 1303
 Query: 607 --EGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK 664
 EGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK
 Sbjct: 1304 AQEGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK 1363
 Query: 665 ELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLGLELI 724
 ELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS EDDAIVLDDATSFNHEESLGLELI
 Sbjct: 1364 ELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS SEDDAIVLDDATSFNHEESLGLELI 1423
 Query: 725 HEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 784
 HEESDAPLLPPRVYSTENHQ HHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS
 Sbjct: 1424 HEESDAPLLPPRVYSTENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 1483
 Query: 785 MPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 844
 MP LAGV ESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS
 Sbjct: 1484 MPALAGVPTAESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 1543
 Query: 845 DGFIVPPNKDGT PPEGSSKGPAHLVTS L 872
 DGFIVPPNKDGT PPEGSSKGPAHLVTS L
 Sbjct: 1544 DGFIVPPNKDGT PPEGSSKGPAHLVTS L 1571

☐ >gi|7513502|pir|T18389 latrophilin-3, splice variant abaf, brain-specific - bov
 gi|4164053|gb|AAD05321.1| (AF111085) latrophilin 3 splice variant abaf [Bos taurus]
 Length = 1503

Score = 1620 bits (4195), Expect = 0.0
 Identities = 807/928 (86%), Positives = 810/928 (86%), Gaps = 56/928 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
 Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK 635

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
 NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
 Sbjct: 696 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 755

Query: 168 STENASMKGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
 STENASMKGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
 Sbjct: 756 STENASMKGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 815

Query: 228 PNCFSWSYSKRTMTGYWSTNGCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 287
 PNCFSWSYSKRTMTGYWST GCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL
 Sbjct: 816 PNCFSWSYSKRTMTGYWSTQGCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 875

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXXXXXRGNSDRNTIHKNLCSLFAELLFLIGINRTD 347
 LLDVITWVG RGL SDRNTIHKNLCSLFAELLFLIGINRTD
 Sbjct: 876 LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSLFAELLFLIGINRTD 935

Query: 348 QPIACXXXXXXXXXXXXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 407
 QPIAC TWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV
 Sbjct: 936 QPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 995

Query: 408 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVIFLGIALYKMFHHTAILKP 467
 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVIFLGIALYKMFHHTAILKP
 Sbjct: 996 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVIFLGIALYKMFHHTAILKP 1055

Query: 468 ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
 ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
 Sbjct: 1056 ESGCLDNIKSWVIGAIALLCLLGLTWAFLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1115

Query: 528 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIRRMWNDTVRK 587
 VLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTSGRTPGRYSTGS SRIRRMWNDTVRK
 Sbjct: 1116 VLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTSGRTPGRYSTGSQSRIRRMWNDTVRK 1175

Query: 588 QSESSFITGDINSSASLNR----- 606
 QSESSFITGDINSSASLNR
 Sbjct: 1176 QSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNNPYNTLLGEPACNNPSVSMYN 1235

Query: 607 --EGLLNARDTSMVDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK 664
 EGLLNARDTSMVDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK
 Sbjct: 1236 AQEGLLNARDTSMVDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK 1295

Query: 665 ELTSNYIPSYLNNHERSSEQNRNLMNKLVNNLGSGREDDAIVLDDATSFNHEESLGLELI 724
 ELTSNYIPSYLNNHERSSEQNRNLMNKLVNNLGSG EDDAIVLDDATSFNHEESLGLELI
 Sbjct: 1296 ELTSNYIPSYLNNHERSSEQNRNLMNKLVNNLGSGSEDDAIVLDDATSFNHEESLGLELI 1355

Query: 725 HEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 784
 HEESDAPLLPPRVYSTENHQ HHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS
 Sbjct: 1356 HEESDAPLLPPRVYSTENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 1415

Query: 785 MPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 844
 MP LAGV ESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS
 Sbjct: 1416 MPALAGVPTAESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 1475

Query: 845 DGFIVPPNKDGTPEGSSKGAHLVTS 872
 DGFIVPPNKDGTPEGSSKGAHLVTS
 Sbjct: 1476 DGFIVPPNKDGTPEGSSKGAHLVTS 1503

☐ >gi|7513949|pir|T17198 CL3BA protein - rat
 gi|3695141|gb|AAC62663.1 (AF081157) CL3BA [Rattus norvegicus]
 Length = 1527

Score = 1618 bits (4189), Expect = 0.0
 Identities = 791/885 (89%), Positives = 801/885 (90%), Gaps = 13/885 (1%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNK----- 48
 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNK
 Sbjct: 643 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 702

Query: 49 -AMVETVNNLLQPQALNAWRDLTTS DQLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETVNNLLQPQALNAWRDLTTS DQLRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 703 QAMVETVNNLLQPQALNAWRDLTTS DQLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 762

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
 NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
 Sbjct: 763 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 822

Query: 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
 STENASMKLGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
 Sbjct: 823 STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 882

Query: 228 PNCSEFWSYSKRTMTGYWSTNGCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 287
 PNCSEFWSYSKRTMTGYWST GCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL
 Sbjct: 883 PNCSEFWSYSKRTMTGYWSTQGCRLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 942

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
 LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD
 Sbjct: 943 LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 1002

Query: 348 QPIACXXXXXXXXXXXXXXXXXTW MFLEGVQLYIMLVEVFSEHSRRKYFYLVGYGMPALIV 407
 QPIAC TW MFLEGVQLYIMLVEVFSEHSRRKYFYLVGYGMPALIV
 Sbjct: 1003 QPIACAVFAALLHFFFLAAFTW MFLEGVQLYIMLVEVFSEHSRRKYFYLVGYGMPALIV 1062

Query: 408 AVSAAVDYRSYGTDKVCWLRLD TYFIW SFIGPATLIIMLN VIFLGIALYKMFHHTAILKP 467
 AVSAAVDYRSYGTDKVCWLRLD TYFIW SFIGPATLIIMLN VIFLGIALYKMFHHTAILKP
 Sbjct: 1063 AVSAAVDYRSYGTDKVCWLRLD TYFIW SFIGPATLIIMLN VIFLGIALYKMFHHTAILKP 1122

Query: 468 ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
 ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
 Sbjct: 1123 ESGCLDNIKSWVIGAIAL LCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1182

Query: 528 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGSNSRIRRMWNDTVRK 587
 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGS SRIRRMWNDTVRK
 Sbjct: 1183 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGSQSRIIRRMWNDTVRK 1242

Query: 588 QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQII 647
 QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIA GEYLSNCVQII
 Sbjct: 1243 QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIAGGEYLSNCVQII 1302

Query: 648 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVL 707
 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRN+MNKL V+NLGSG EDDAIVL
 Sbjct: 1303 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNMMNKLVDNLGSGSEDDAIVL 1362

Query: 708 DDATSFNHEESLGLLELIHEESDAPLLP PRVYSTENHQP HHY+RRR+PQDHSESFFPLLTN 767
 DDA SFNHEESLGLLELIHEESDAPLLP PRVYST+NHQP HHY+RRR+PQDHSESFFPLLT+
 Sbjct: 1363 DDAASFNHEESLGLLELIHEESDAPLLP PRVYSTDNHQP HHYSRRRLPQDHSESFFPLLT 1422

Query: 768 EHTEDLQSPHRDSLYTSMPTLAGVAATESVTTSTQT EPPPAKCGDAEDVYYKSM PNLSGR 827
 EHTED QSPHRDSLYTSMPT LAGV A +SVTTSTQTE AK GDAEDVYYKSM PNLSGR
 Sbjct: 1423 EHTEDPQSPHRDSLYTSM PALAGVPAADSVTTSTQTEAAAAKGGDAEDVYYKSM PNLSGR 1482

Query: 828 NHVHQLHTYYQLGRGSSDGFIVPPNKG TTPPEGSSSKGPAHLVTSL 872
 NHVH LH YYQLGRGSSDGFIVPPNKG PEG+SKGPAHLVTSL

Sbjct: 1483 NHVHPLHAYYQLGRGSSDGFIVPPNKDGASPEGTSKGAHLVTSL 1527

☐ >gi|7513511|pir||T18407 latrophilin-3, splice variant bbbf, brain-specific - bov
gi|4164071|gb|AAD05330.1 (AF111094) latrophilin 3 splice variant bbbf [Bos taurus
Length = 1580

Score = 1615 bits (4181), Expect = 0.0

Identities = 807/937 (86%), Positives = 810/937 (86%), Gaps = 65/937 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK
Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
Sbjct: 764 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 823

Query: 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
STENASMKLGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
Sbjct: 824 STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 883

Query: 228 PNCSEFWSYSKRTMTGYWSTNGCRLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL 287
PNCSEFWSYSKRTMTGYWST GCRLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL
Sbjct: 884 PNCSEFWSYSKRTMTGYWSTQGCRLLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL 943

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXXXXRGLNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD
Sbjct: 944 LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 1003

Query: 348 QPIACXXXXXXXXXXXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 407
QPIAC TWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV
Sbjct: 1004 QPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 1063

Query: 408 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 467
AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP
Sbjct: 1064 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 1123

Query: 468 ESGCLDN-----IKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLN 518
ESGCLDN IKSWVI MYINESTVIMAYLFTIFNSL
Sbjct: 1124 ESGCLDNINYEDNRPFIKSWVIGAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQ 1183

Query: 519 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGSRTPGRYSTGSNSRIR 578
GMFIFIFHCVLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTSGSRTPGRYSTGS SRIR
Sbjct: 1184 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTSGSRTPGRYSTGSQSRIR 1243

Query: 579 RMWNDTVRKQSESSFITGDINSSASLNR----- 606
RMWNDTVRKQSESSFITGDINSSASLNR
Sbjct: 1244 RMWNDTVRKQSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNNPYNTLLGEPAVC 1303

Query: 607 -----EGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNE 655
EGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNE
Sbjct: 1304 NNPSVSMYNAQEGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNE 1363

Query: 656 TALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNL GSGREDDAIVLDDATSFNH 715
TALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNL GSG EDDAIVLDDATSFNH
Sbjct: 1364 TALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNL GSG SEDDAIVLDDATSFNH 1423

Query: 716 EESLGLLELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQS 775
EESLGLLELIHEESDAPLLPPRVYSTENHQ HHYTRRRIPQDHSESFFPLLTNEHTEDLQS
Sbjct: 1424 EESLGLLELIHEESDAPLLPPRVYSTENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQS 1483

Query: 776 PHRDSLYTSMPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHT 835
 PHRDSLYTSMP LAGV ESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHT
 Sbjct: 1484 PHRDSLYTSMPALAGVPTAESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHT 1543

Query: 836 YYQLGRGSSDGFIVPPNKGTPPEGSSKGAHLVTS 872
 YYQLGRGSSDGFIVPPNKGTPPEGSSKGAHLVTS
 Sbjct: 1544 YYQLGRGSSDGFIVPPNKGTPPEGSSKGAHLVTS 1580

☐ >gi|7513946|pir|T17186 CL3AA protein - rat
 gi|3695135|gb|AAC62660.1| (AF081154) CL3AA [Rattus norvegicus]
 Length = 1459

Score = 1613 bits (4178), Expect = 0.0
 Identities = 791/885 (89%), Positives = 801/885 (90%), Gaps = 13/885 (1%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK
 Sbjct: 575 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 634

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 635 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLDVVEESAFVLADNLLKTDIVRENTD 694

Query: 108 NIKLEVARLSTEGNLEDLKFPEMNGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
 NI+LEVARLSTEGNLEDLKFPEM GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
 Sbjct: 695 NIQLEVARLSTEGNLEDLKFPEMNGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 754

Query: 168 STENASMKLGTALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
 STENASMKLGTAA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
 Sbjct: 755 STENASMKLGTAASTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 814

Query: 228 PNCFSWSYSKRTMTGYWSTNGCRLLTTNKTHTTSCNHLTNFAVLMAHVEVKHSDAVHDL 287
 PNCFSWSYSKRTMTGYWST GCRLLTTNKTHTTSCNHLTNFAVLMAHVEVKHSDAVHDL
 Sbjct: 815 PNCFSWSYSKRTMTGYWSTQGCRLTTNKTHTTSCNHLTNFAVLMAHVEVKHSDAVHDL 874

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXRGNSDRNTIHKNLCSLFFVAELLFLIGINRTD 347
 LLDVITWVG RGL SDRNTIHKNLCSLFFVAELLFLIGINRTD
 Sbjct: 875 LLDVITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHKNLCSLFFVAELLFLIGINRTD 934

Query: 348 QPIACXXXXXXXXXXXXXXXXXTWMFLEGVQLYIMLVEVFSEHSRRKYFYLVGYGMPALIV 407
 QPIAC TWMFLEGVQLYIMLVEVFSEHSRRKYFYLVGYGMPALIV
 Sbjct: 935 QPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFSEHSRRKYFYLVGYGMPALIV 994

Query: 408 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVIPLGIALYKMFHHTAILKP 467
 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVIPLGIALYKMFHHTAILKP
 Sbjct: 995 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVIPLGIALYKMFHHTAILKP 1054

Query: 468 ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
 ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
 Sbjct: 1055 ESGCLDNIKSWVIGAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1114

Query: 528 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIRRMWNDTVRK 587
 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGS SRIRRMWNDTVRK
 Sbjct: 1115 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSQSRIRRMWNDTVRK 1174

Query: 588 QSESSFITGDINSSASLNREGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVQII 647
 QSESSFITGDINSSASLNREGLLNARDTSVMDTLPNGNHGNSYSIA GEYLSNCVQII
 Sbjct: 1175 QSESSFITGDINSSASLNREGLLNARDTSVMDTLPNGNHGNSYSIAGGEYLSNCVQII 1234

Query: 648 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKLVDNLGSGREDDAIVL 707
 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRN+MNKLVDNLGSGREDDAIVL
 Sbjct: 1235 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNMMNKLVDNLGSGREDDAIVL 1294

Query: 708 DDATSFNHEESLGLLEIHEESDAPLLPPRVYSTENHQP HHY+RRR+PQDHSESFFPLLTN 767
 DDA SFNHEESLGLLEIHEESDAPLLPPRVYST+NHQP HHY+RRR+PQDHSESFFPLLT+

Sbjct: 1295 DDAASFNHEESLGLELIHEESDAPLLPPRVYSTDNHQPHYSRRRLPQDHSESFFPLLT 1354

Query: 768 EHTEDLQSPHRDSLYTSMPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGS 827
EHTED QSPHRDSLYTSMPT LAGV A +SVTTSTQTE AK GDAEDVYYKSMPNLGS

Sbjct: 1355 EHTEDPQSPHRDSLYTSMPALAGVPAADSVTTSTQTEAAAAKGGDAEDVYYKSMPNLGS 1414

Query: 828 NHVHQLHTYYQLGRGSSDGFIVPPNKGDTPEGSSKGAHLVTSL 872
NHVH LH YYQLGRGSSDGFIVPPNKG PEG+SKGAHLVTSL

Sbjct: 1415 NHVHPLHAYYQLGRGSSDGFIVPPNKGASPEGTSKGAHLVTSL 1459

☐ >gi|7513505|pir|T18392 latrophilin-3, splice variant abbf, brain-specific - bov
gi|4164059|gb|AAD05324.1 (AF111088) latrophilin 3 splice variant abbf [Bos tauru
Length = 1512

Score = 1611 bits (4171), Expect = 0.0
Identities = 807/937 (86%), Positives = 810/937 (86%), Gaps = 65/937 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK

Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL

Sbjct: 696 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 755

Query: 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
STENASMKLGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN

Sbjct: 756 STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 815

Query: 228 PNCSFWSYSKRTMTGYWSTNGCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 287
PNCSFWSYSKRTMTGYWST GCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL

Sbjct: 816 PNCSFWSYSKRTMTGYWSTQGCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 875

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXXXXRGLNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD

Sbjct: 876 LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 935

Query: 348 QPIACXXXXXXXXXXXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYL VGYGMPALIV 407
QPIAC TWMFLEGVQLYIMLVEVFESHSRRKYFYL VGYGMPALIV

Sbjct: 936 QPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYL VGYGMPALIV 995

Query: 408 AVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 467
AVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP

Sbjct: 996 AVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 1055

Query: 468 ESGCLDN-----IKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLN 518
ESGCLDN IKSWVI MYINESTVIMAYLFTIFNSL

Sbjct: 1056 ESGCLDNINYEDNRPFIKSWVIGAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQ 1115

Query: 519 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTTPGRYSTGSNSRIR 578
GMFIFIFHCVLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTS GSRTTPGRYSTGS SRIR

Sbjct: 1116 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTS GSRTTPGRYSTGSQSRI 1175

Query: 579 RMWNDTVRKQSESSFITGDINSSASLNR----- 606
RMWNDTVRKQSESSFITGDINSSASLNR

Sbjct: 1176 RMWNDTVRKQSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNPNPYNTLLGEP 1235

Query: 607 -----EGLLN NARDTSVMDTLP LN GNHGN SYSIASGEYLSNCVQIIDRGYNHNE 655
EGLLN NARDTSVMDTLP LN GNHGN SYSIASGEYLSNCVQIIDRGYNHNE

Sbjct: 1236 NNPSVSMYNAQEGLLN NARDTSVMDTLP LN GNHGN SYSIASGEYLSNCVQIIDRGYNHNE 1295



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NCBI Conserved Domain Search

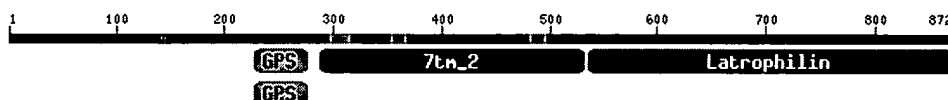
[New Search](#) [PubMed](#) [Nucleotide](#) [Protein](#) [Structure](#) [CDD](#) [Taxonomy](#) [Help?](#)

RPS-BLAST 2.2.3 [Apr-24-2002]

Query= local sequence:
(872 letters)

Database: oasis_sap.v1.58
4540 PSSMs; 885,521 total columns

Click on boxes for multiple alignments



Show Domain Relatives

PSSMs producing significant alignments:

Score E
(bits) value

| | | |
|--|----------------------|------------------------|
| gnl CDD 2865 pfam02354, Latrophilin, Latrophilin Cytoplasmic C-terminal reg... | 485 | 2e-138 |
| gnl CDD 571 pfam00002, 7tm_2, 7 transmembrane receptor (Secretin family) | 217 | 2e-57 |
| gnl CDD 2352 pfam01825, GPS, Latrophilin/CL-1-like GPS domain. Domain prese... | 75.4 | 8e-15 |
| gnl CDD 3874 smart00303, GPS, G-protein-coupled receptor proteolytic site d... | 74.3 | 2e-14 |

[gnl|CDD|2865](#), pfam02354, Latrophilin, Latrophilin Cytoplasmic C-terminal region. This family consists of the cytoplasmic C-terminal region in latrophilin. Latrophilin is a synaptic Ca²⁺ independent alpha-latrotoxin (LTX) receptor and is a novel member of the secretin family of G-protein coupled receptors that are involved in secretion. Latrophilin mRNA is present only in neuronal tissue. Latrophillin interacts with G-alpha O.

CD-Length = 370 residues, 100.0% aligned
Score = 485 bits (1250), Expect = 2e-138

| | | |
|------------|--|-----|
| Query: 535 | KEYGKCLR-THCCSGKSTESSIGSGKTSRTPGRYSTGSNSRIRRMWNDTVRKQSESSF | 593 |
| Sbjct: 1 | KEYHKCSRGPCCSGLPTESQKDSGKQSGSRTPRLYSTGCQSRIRRMWNDTVRKQSESSF | 60 |
| | | |
| Query: 594 | ITGDINSSASLNR-----EGLL | 610 |
| Sbjct: 61 | IAGDINSTPTLNRGTMGNHLLTNPLLRPHGTNNPYNTLLAESVVCNPPSPVPVFNPSGYSYL | 120 |
| | | |
| Query: 611 | NNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILKELTSNY | 670 |
| Sbjct: 121 | NNGRDTSGMMDTLPLNGNFNNSYSLSRGDYPPGDVQEPDRGRNLNDTAFEKMIISELVHNN | 180 |
| | | |
| Query: 671 | IPSYLNNHERSSEQNRNLMNKLVNNLGSGREDDAIVLDDATSFNHEESLGLLELIHEESDA | 730 |
| Sbjct: 181 | LRGASGGHK--GPPPEPPVPPVPG--GSVSEDDAIVP-DATSFNHADRAGLELLHKELEA | 235 |
| | | |
| Query: 731 | PLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLNEHTEDLQSPHRDSLYTSMPTLAG | 790 |
| Sbjct: 236 | PLLPPRT----AHSLLYQSDRRIPLDESESECTAELTAESRELLQSPGRDSLYTSMPLNRD | 291 |
| | | |
| Query: 791 | VAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSSDGFIVP | 850 |
| Sbjct: 292 | SPYPESSPEPNEALPPPPAPPGPEDIYYKSMPNLGAR---NQLQGYQVRRGSSDGYIAP | 348 |

Query: 851 PNKDGTPPEGSSKGPAHLVTSL 872
Sbjct: 349 PNKEGPGPEGDGQGPMQLVTSL 370

gnl|CDD|571, pfam00002, 7tm_2, 7 transmembrane receptor (Secretin family).

CD-Length = 249 residues, 100.0% aligned
Score = 217 bits (554), Expect = 2e-57

Query: 286 DLLLDVITWVGILLSLVCLLICIFTFCFFRGLNSDRNTIHKNLCSLFAELLFLIGINR 345
Sbjct: 1 ALLLSVIYTVGYSLVCLLLAIAIFLFFRKLRCTRNIIHLNLFSLILRALSFLIGDAV 60

Query: 346 TDQPIA--CAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMP 403
Sbjct: 61 LLNSGGLGCKVAVFLHYFFLANFFWMLVEGLYLYTLLVETFFSERLRLLWYLLIGWGP 120

Query: 404 ALIVAVSAAVDYRSYGTKVCWLRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTA 463
Sbjct: 121 AVVVGIWALVRPKGYGNEGCCWLSNEGGEFWWIFKGPVLLIILVNFIFFINILRVLVQKLR 180

Query: 464 ILKPESGCLDNIKSWVIGAIALLCGLTWAFGLMYINE-STVIMAYLFTIFNSLNGMFI 522
Sbjct: 181 --SPQTGKTDLYRKLVKSTLVLLPLLGVTWILFLFAPESQSSLVFLYLFLLNSFQGFV 238

Query: 523 FIFHCVLQKKV 533
Sbjct: 239 AVLYCFLNGEV 249

gnl|CDD|2352, pfam01825, GPS, Latrophilin/CL-1-like GPS domain. Domain present in latrophilin/CL-1, sea urchin REJ and polycystin.

CD-Length = 49 residues, 100.0% aligned
Score = 75.4 bits (185), Expect = 8e-15

Query: 226 FNPNC SFWSYSKRTMTGYWSTNGCRLLTNKTHTTCSNHLTNFAVLMAHVEV 278
Sbjct: 1 SNPICVFWEDESS----GVWSTRGCELVETSKTHTTCSNHLTSFAVLMDVPPN 49

gnl|CDD|3874, smart00303, GPS, G-protein-coupled receptor proteolytic site domain; Present in latrophilin/CL-1, sea urchin REJ and polycystin.

CD-Length = 49 residues, 100.0% aligned
Score = 74.3 bits (182), Expect = 2e-14

Query: 226 FNPNC SFWSYSKRTMTGYWSTNGCRLLTNKTHTTCSNHLTNFAVLMAHVEV 278
Sbjct: 1 FNPICVFWEDESS----GEWSTRGCELLETSSSTHTTCSNHLTSFAVLMDVPPI 49

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